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Reviewer: Keisha Douglas

Timestamp: [year=2008; month=2; day=28; hr=18; min=14; sec=35; ms=893;]

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Application No: 10510628 Version No: 2.0

Input Set:

Output Set:

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Finished: 2008-02-14 17:17:24.227
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Total Warnings: 0
Total Errors: 0
No. of SeqIDs Defined: 4
Actual SeqID Count: 4

SEQUENCE LISTING

<110> HEGEMANN, Peter

<120> USE OF BIOLOGICAL PHOTORECEPTORS AS DIRECTLY LIGHT-CONTROLLED
ION CHANNELS

<130> 231181

<140> 10510628

<141> 2005-05-09

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 712

<212> PRT

<213> Chlamydomonas reinhardtii

<220>

<223> Amino acid sequence of CHOP-1 from
Chlamydomonas reinhardtii

<400> 1

Met	Ser	Arg	Arg	Pro	Trp	Leu	Leu	Ala	Leu	Ala	Leu	Ala	Val	Ala	Leu
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Ala	Ala	Gly	Ser	Ala	Gly	Ala	Ser	Thr	Gly	Ser	Asp	Ala	Thr	Val	Pro
		20						25					30		

Val	Ala	Thr	Gln	Asp	Gly	Pro	Asp	Tyr	Val	Phe	His	Arg	Ala	His	Glu
		35						40				45			

Arg	Met	Leu	Phe	Gln	Thr	Ser	Tyr	Thr	Leu	Glu	Asn	Asn	Gly	Ser	Val
	50					55						60			

Ile	Cys	Ile	Pro	Asn	Asn	Gly	Gln	Cys	Phe	Cys	Leu	Ala	Trp	Leu	Lys
65					70					75					80

Ser	Asn	Gly	Thr	Asn	Ala	Glu	Lys	Leu	Ala	Ala	Asn	Ile	Leu	Gln	Trp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

				85				90				95			
Ile	Thr	Phe	Ala	Leu	Ser	Ala	Leu	Cys	Leu	Met	Phe	Tyr	Gly	Tyr	Gln
100				105				110							
Thr	Trp	Lys	Ser	Thr	Cys	Gly	Trp	Glu	Glu	Ile	Tyr	Val	Ala	Thr	Ile
115				120				125							
Glu	Met	Ile	Lys	Phe	Ile	Ile	Glu	Tyr	Phe	His	Glu	Phe	Asp	Glu	Pro
130				135				140							
Ala	Val	Ile	Tyr	Ser	Ser	Asn	Gly	Asn	Lys	Thr	Val	Trp	Leu	Arg	Tyr
145				150				155				160			
Ala	Glu	Trp	Leu	Leu	Thr	Cys	Pro	Val	Ile	Leu	Ile	His	Leu	Ser	Asn
165				170				175							
Leu	Thr	Gly	Leu	Ala	Asn	Asp	Tyr	Asn	Lys	Arg	Thr	Met	Gly	Leu	Leu
180				185				190							
Val	Ser	Asp	Ile	Gly	Thr	Ile	Val	Trp	Gly	Thr	Thr	Ala	Ala	Leu	Ser
195				200				205							
Lys	Gly	Tyr	Val	Arg	Val	Ile	Phe	Phe	Leu	Met	Gly	Leu	Cys	Tyr	Gly
210				215				220							
Ile	Tyr	Thr	Phe	Phe	Asn	Ala	Ala	Lys	Val	Tyr	Ile	Glu	Ala	Tyr	His
225				230				235				240			
Thr	Val	Pro	Lys	Gly	Ile	Cys	Arg	Asp	Leu	Val	Arg	Tyr	Leu	Ala	Trp
245				250				255							
Leu	Tyr	Phe	Cys	Ser	Trp	Ala	Met	Phe	Pro	Val	Leu	Phe	Leu	Leu	Gly
260				265				270							
Pro	Glu	Gly	Phe	Gly	His	Ile	Asn	Gln	Phe	Asn	Ser	Ala	Ile	Ala	His
275				280				285							
Ala	Ile	Leu	Asp	Leu	Ala	Ser	Lys	Asn	Ala	Trp	Ser	Met	Met	Gly	His
290				295				300							
Phe	Leu	Arg	Val	Lys	Ile	His	Glu	His	Ile	Leu	Leu	Tyr	Gly	Asp	Ile
305				310				315				320			
Arg	Lys	Lys	Gln	Lys	Val	Asn	Val	Ala	Gly	Gln	Glu	Met	Glu	Val	Glu
325				330				335							
Thr	Met	Val	His	Glu	Glu	Asp	Asp	Glu	Thr	Gln	Lys	Val	Pro	Thr	Ala
340				345				350							
Lys	Tyr	Ala	Asn	Arg	Asp	Ser	Phe	Ile	Ile	Met	Arg	Asp	Arg	Leu	Lys
355				360				365							
Glu	Lys	Gly	Phe	Glu	Thr	Arg	Ala	Ser	Leu	Asp	Gly	Asp	Pro	Asn	Gly
370				375				380							
Asp	Ala	Glu	Ala	Asn	Ala	Ala	Ala	Gly	Gly	Lys	Pro	Gly	Met	Glu	Met

385		390		395		400
Gly Lys Met Thr	Gly Met Gly Met Gly Met Gly Ala Gly Met Gly Met					
	405		410		415	
Ala Thr Ile Asp Ser	Gly Arg Val Ile Leu Ala Val Pro Asp Ile Ser					
	420		425		430	
Met Val Asp Phe Phe Arg	Glu Gln Phe Ala Arg Leu Pro Val Pro Tyr					
	435		440		445	
Glu Leu Val Pro Ala Leu	Gly Ala Glu Asn Thr Leu Gln Leu Val Gln					
	450		455		460	
Gln Ala Gln Ser Leu Gly	Gly Cys Asp Phe Val Leu Met His Pro Glu					
	465		470		475	
Phe Leu Arg Asp Arg Ser	Pro Thr Gly Leu Leu Pro Arg Leu Lys Met					
	485		490		495	
Gly Gly Gln Arg Ala Ala	Ala Phe Gly Trp Ala Ala Ile Gly Pro Met					
	500		505		510	
Arg Asp Leu Ile Glu Gly	Ser Gly Val Asp Gly Trp Leu Glu Gly Pro					
	515		520		525	
Ser Phe Gly Ala Gly Ile	Asn Gln Gln Ala Leu Val Ala Leu Ile Asn					
	530		535		540	
Arg Met Gln Gln Ala Lys	Lys Met Gly Met Met Gly Gly Met Gly Met					
	545		550		555	
Gly Met Gly Gly Gly Met	Gly Met Gly Met Gly Met Gly Met Gly Met					
	565		570		575	
Ala Pro Ser Met Asn Ala	Gly Met Thr Gly Gly Met Gly Gly Ala Ser					
	580		585		590	
Met Gly Gly Ala Val Met	Gly Met Gly Met Gly Met Gln Pro Met Gln					
	595		600		605	
Gln Ala Met Pro Ala Met	Ser Pro Met Met Thr Gln Gln Pro Ser Met					
	610		615		620	
Met Ser Gln Pro Ser Ala	Met Ser Ala Gly Gly Ala Met Gln Ala Met					
	625		630		635	
Gly Gly Val Met Pro Ser	Pro Ala Pro Gly Gly Arg Val Gly Thr Asn					
	645		650		655	
Pro Leu Phe Gly Ser Ala	Pro Ser Pro Leu Ser Ser Gln Pro Gly Ile					
	660		665		670	
Ser Pro Gly Met Ala Thr	Pro Pro Ala Ala Thr Ala Ala Pro Ala Ala					
	675		680		685	
Gly Gly Ser Glu Ala Glu	Met Leu Gln Gln Leu Met Ser Glu Ile Asn					

690

695

700

Arg Leu Lys Asn Glu Leu Gly Glu

705

710

<210> 2

<211> 737

<212> PRT

<213> Chlamydomonas reinhardtii

<220>

<223> Amino acid sequence of CHOP-2 from
Chlamydomonas reinhardtii

<400> 2

Met Asp Tyr Gly Gly Ala Leu Ser Ala Val Gly Arg Glu Leu Leu Phe
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Val Thr Asn Pro Val Val Val Asn Gly Ser Val Leu Val Pro Glu Asp
20 25 30

Gln Cys Tyr Cys Ala Gly Trp Ile Glu Ser Arg Gly Thr Asn Gly Ala
35 40 45

Gln Thr Ala Ser Asn Val Leu Gln Trp Leu Ala Ala Gly Phe Ser Ile
50 55 60

Leu Leu Leu Met Phe Tyr Ala Tyr Gln Thr Trp Lys Ser Thr Cys Gly
65 70 75 80

Trp Glu Glu Ile Tyr Val Cys Ala Ile Glu Met Val Lys Val Ile Leu
85 90 95

Glu Phe Phe Phe Glu Phe Lys Asn Pro Ser Met Leu Tyr Leu Ala Thr
100 105 110

Gly His Arg Val Gln Trp Leu Arg Tyr Ala Glu Trp Leu Leu Thr Cys
115 120 125

Pro Val Ile Leu Ile His Leu Ser Asn Leu Thr Gly Leu Ser Asn Asp
130 135 140

Tyr Ser Arg Arg Thr Met Gly Leu Leu Val Ser Asp Ile Gly Thr Ile
145 150 155 160

Val Trp Gly Ala Thr Ser Ala Met Ala Thr Gly Tyr Val Lys Val Ile
165 170 175

Phe Phe Cys Leu Gly Leu Cys Tyr Gly Ala Asn Thr Phe Phe His Ala
180 185 190

Ala	Lys	Ala	Tyr	Ile	Glu	Gly	Tyr	His	Thr	Val	Pro	Lys	Gly	Arg	Cys
195						200						205			
Arg	Gln	Val	Val	Thr	Gly	Met	Ala	Trp	Leu	Phe	Phe	Val	Ser	Trp	Gly
210						215						220			
Met	Phe	Pro	Ile	Leu	Phe	Ile	Leu	Gly	Pro	Glu	Gly	Phe	Gly	Val	Leu
225						230						235			
Ser	Val	Tyr	Gly	Ser	Thr	Val	Gly	His	Thr	Ile	Ile	Asp	Leu	Met	Ser
			245						250			255			
Lys	Asn	Cys	Trp	Gly	Leu	Leu	Gly	His	Tyr	Leu	Arg	Val	Leu	Ile	His
			260						265			270			
Glu	His	Ile	Leu	Ile	His	Gly	Asp	Ile	Arg	Lys	Thr	Thr	Lys	Leu	Asn
275						280						285			
Ile	Gly	Gly	Thr	Glu	Ile	Glu	Val	Glu	Thr	Leu	Val	Glu	Asp	Glu	Ala
290						295						300			
Glu	Ala	Gly	Ala	Val	Asn	Lys	Gly	Thr	Gly	Lys	Tyr	Ala	Ser	Arg	Glu
305						310						315			
Ser	Phe	Leu	Val	Met	Arg	Asp	Lys	Met	Lys	Glu	Lys	Gly	Ile	Asp	Val
			325						330			335			
Arg	Ala	Ser	Leu	Asp	Asn	Ser	Lys	Glu	Val	Glu	Gln	Glu	Gln	Ala	Ala
			340						345			350			
Arg	Ala	Ala	Met	Met	Met	Met	Asn	Gly	Asn	Gly	Met	Gly	Met	Gly	Met
355						360						365			
Gly	Met	Asn	Gly	Met	Asn	Gly	Met	Gly	Gly	Met	Asn	Gly	Met	Ala	Gly
370						375						380			
Gly	Ala	Lys	Pro	Gly	Leu	Glu	Leu	Thr	Pro	Gln	Leu	Gln	Pro	Gly	Arg
385						390						395			
Val	Ile	Leu	Ala	Val	Pro	Asp	Ile	Ser	Met	Val	Asp	Phe	Phe	Arg	Glu
			405						410			415			
Gln	Phe	Ala	Gln	Leu	Ser	Val	Thr	Tyr	Glu	Leu	Val	Pro	Ala	Leu	Gly
			420						425			430			
Ala	Asp	Asn	Thr	Leu	Ala	Leu	Val	Thr	Gln	Ala	Gln	Asn	Leu	Gly	Gly
435						440						445			
Val	Asp	Phe	Val	Leu	Ile	His	Pro	Glu	Phe	Leu	Arg	Asp	Arg	Ser	Ser
450						455						460			
Thr	Ser	Ile	Leu	Ser	Arg	Leu	Arg	Gly	Ala	Gly	Gln	Arg	Val	Ala	Ala
465						470						475			
Phe	Gly	Trp	Ala	Gln	Leu	Gly	Pro	Met	Arg	Asp	Leu	Ile	Glu	Ser	Ala
			485						490			495			

Asn Leu Asp Gly Trp Leu Glu Gly Pro Ser Phe Gly Gln Gly Ile Leu
500 505 510

Pro Ala His Ile Val Ala Leu Val Ala Lys Met Gln Gln Met Arg Lys
515 520 525

Met Gln Gln Met Gln Gln Ile Gly Met Met Thr Gly Gly Met Asn Gly
530 535 540

Met Gly Gly Gly Met Gly Gly Gly Met Asn Gly Met Gly Gly Gly Asn
545 550 555 560

Gly Met Asn Asn Met Gly Asn Gly Met Gly Gly Gly Met Gly Asn Gly
565 570 575

Met Gly Gly Asn Gly Met Asn Gly Met Gly Gly Gly Asn Gly Met Asn
580 585 590

Asn Met Gly Gly Asn Gly Met Ala Gly Asn Gly Met Gly Gly Gly Met
595 600 605

Gly Gly Asn Gly Met Gly Gly Ser Met Asn Gly Met Ser Ser Gly Val
610 615 620

Val Ala Asn Val Thr Pro Ser Ala Ala Gly Gly Met Gly Gly Met Met
625 630 635 640

Asn Gly Gly Met Ala Ala Pro Gln Ser Pro Gly Met Asn Gly Gly Arg
645 650 655

Leu Gly Thr Asn Pro Leu Phe Asn Ala Ala Pro Ser Pro Leu Ser Ser
660 665 670

Gln Leu Gly Ala Glu Ala Gly Met Gly Ser Met Gly Gly Met Gly Gly
675 680 685

Met Ser Gly Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly Ala
690 695 700

Gly Ala Ala Thr Thr Gln Ala Ala Gly Gly Asn Ala Glu Ala Glu Met
705 710 715 720

Leu Gln Asn Leu Met Asn Glu Ile Asn Arg Leu Lys Arg Glu Leu Gly
725 730 735

Glu

<210> 3

<211> 259

<212> PRT

<213> Halobacterium salinarum

<220>

<223> Amino acid sequence of bacteriorhodopsin from
Halobacterium salinarum

<400> 3

Met Leu Pro Thr Ala Val Glu Gly Val Ser Gln Ala Gln Ile Thr Gly
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Arg Pro Glu Trp Ile Trp Leu Ala Leu Gly Thr Ala Leu Met Gly Leu
20 25 30

Gly Thr Leu Tyr Phe Leu Val Lys Gly Met Gly Val Ser Asp Pro Asp
35 40 45

Ala Lys Lys Phe Tyr Ala Ile Thr Thr Leu Val Pro Ala Ile Ala Phe
50 55 60

Thr Met Tyr Leu Ser Met Leu Leu Gly Tyr Gly Leu Thr Met Val Pro
65 70 75 80

Phe Gly Gly Glu Gln Asn Pro Ile Tyr Trp Ala Arg Tyr Ala Asp Trp
85 90 95

Leu Phe Thr Thr Pro Leu Leu Leu Leu Asp Leu Ala Leu Leu Val Asp
100 105 110

Ala Asp Gln Gly Thr Ile Leu Ala Leu Val Gly Ala Asp Gly Ile Met
115 120 125

Ile Gly Thr Gly Leu Val Gly Ala Leu Thr Lys Val Tyr Ser Tyr Arg
130 135 140

Phe Val Trp Trp Ala Ile Ser Thr Ala Ala Met Leu Tyr Ile Leu Tyr
145 150 155 160

Val Leu Phe Phe Gly Phe Thr Ser Lys Ala Glu Ser Met Arg Pro Glu
165 170 175

Val Ala Ser Thr Phe Lys Val Leu Arg Asn Val Thr Val Val Leu Trp
180 185 190

Ser Ala Tyr Pro Val Val Trp Leu Ile Gly Ser Glu Gly Ala Gly Ile
195 200 205

Val Pro Leu Asn Ile Glu Thr Leu Leu Phe Met Val Leu Asp Val Ser
210 215 220

Ala Lys Val Gly Phe Gly Leu Ile Leu Leu Arg Ser Arg Ala Ile Phe
225 230 235 240

Gly Glu Ala Glu Ala Pro Glu Pro Ser Ala Gly Asp Gly Ala Ala Ala
245 250 255

Thr Ser Asp

<210> 4
<211> 315
<212> PRT
<213> Chlamydomonas reinhardtii

<220>

<223> Amino acid sequence of the CHOP2-315/H134R mutant

<400> 4

Met Asp Tyr Gly Gly Ala Leu Ser Ala Val Gly Arg Glu Leu Leu Phe
1 5 10 15

Val Thr Asn Pro Val Val Val Asn Gly Ser Val Leu Val Pro Glu Asp
20 25 30

Gln Cys Tyr Cys Ala Gly Trp Ile Glu Ser Arg Gly Thr Asn Gly Ala
35 40 45

Gln Thr Ala Ser Asn Val Leu Gln Trp Leu Ala Ala Gly Phe Ser Ile
50 55 60

Leu Leu Leu Met Phe Tyr Ala Tyr Gln Thr Trp Lys Ser Thr Cys Gly
65 70 75 80

Trp Glu Glu Ile Tyr Val Cys Ala Ile Glu Met Val Lys Val Ile Leu
85 90 95

Glu Phe Phe Phe Glu Phe Lys Asn Pro Ser Met Leu Tyr Leu Ala Thr
100 105 110

Gly His Arg Val Gln Trp Leu Arg Tyr Ala Glu Trp Leu Leu Thr Cys
115 120 125

Pro Val Ile Leu Ile Arg Leu Ser Asn Leu Thr Gly Leu Ser Asn Asp
130 135 140

Tyr Ser Arg Arg Thr Met Gly Leu Leu Val Ser Asp Ile Gly Thr Ile
145 150 155 160

Val Trp Gly Ala Thr Ser Ala Met Ala Thr Gly Tyr Val Lys Val Ile

165

170

175

Phe Phe Cys Leu Gly Leu Cys Tyr Gly Ala Asn Thr Phe Phe His Ala
180 185 190

Ala Lys Ala Tyr Ile Glu Gly Tyr His Thr Val Pro Lys Gly Arg Cys
195 200 205

Arg Gln Val Val Thr Gly Met Ala Trp Leu Phe Phe Val Ser Trp Gly
210 215 220

Met Phe Pro Ile Leu Phe Ile Leu Gly Pro Glu Gly Phe Gly Val Leu
225 230 235 240

Ser Val Tyr Gly Ser Thr Val Gly His Thr Ile Ile Asp Leu Met Ser
245 250 255

Lys Asn Cys Trp Gly Leu Leu Gly His Tyr Leu Arg Val Leu Ile His
260 265 270

Glu His Ile Leu Ile His Gly Asp Ile Arg Lys Thr Thr Lys Leu Asn
275 280